

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: WEI, YING-FEI
KREIDER, BRENT
ROSEN, CRAIG

(ii) TITLE OF INVENTION: CHEMOKINE BETA 15

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
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(C) CITY: WASHINGTON
(D) STATE: D.C.
(E) COUNTRY: US
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: (To Be Assigned)
(B) FILING DATE: HERewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/019,837
(B) FILING DATE: 17-JUN-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Steffe, Eric K.
(B) REGISTRATION NUMBER: 36,688
(C) REFERENCE/DOCKET NUMBER: 1488.0420001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 989 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

06674460 061697

64

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 88..534

(ix) FEATURE:

(A) NAME/KEY: sig_peptide
(B) LOCATION: 88..147

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 148..534

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGGCGGGCA TCAGCTCCCT TGACCCAGTG GATATCGGTG GCCCCGTTAT TCGTCCAGGT	60
GCCCAGGGAG GAGGACCCGC CTGCAGC ATG AAC CTG TGG CTC CTG GCC TGC	111
Met Asn Leu Trp Leu Leu Ala Cys	
-20 -15	
CTG GTG GCC GGC TTC CTG GGA GCC TGG GCC CCC GCT GTC CAC ACC CAA	159
Leu Val Ala Gly Phe Leu Gly Ala Trp Ala Pro Ala Val His Thr Gln	
-10 -5 1	
GGT GTC TTT GAG GAC TGC TGC CTG GCC TAC CAC TAC CCC ATT GGG TGG	207
Gly Val Phe Glu Asp Cys Cys Leu Ala Tyr His Tyr Pro Ile Gly Trp	
5 10 15 20	
GCT GTG CTC CGG CGC GCC TGG ACT TAC CGG ATC CAG GAG GTG AGC GGG	255
Ala Val Leu Arg Arg Ala Trp Thr Tyr Arg Ile Gln Glu Val Ser Gly	
25 30 35	
AGC TGC AAT CTG CCT GCT GCG ATA TTC TAC CTC CCC AAG AGA CAC AGG	303
Ser Cys Asn Leu Pro Ala Ala Ile Phe Tyr Leu Pro Lys Arg His Arg	
40 45 50	
AAG GTG TGT GGG AAC CCC AAA AGC AGG GAG GTG CAG AGA GCC ATG AAG	351
Lys Val Cys Gly Asn Pro Lys Ser Arg Glu Val Gln Arg Ala Met Lys	
55 60 65	
CTC CTG GAT GCT CGA AAT AAG GTT TTT GCA AAG CTC CAC CAC AAC ACG	399
Leu Leu Asp Ala Arg Asn Lys Val Phe Ala Lys Leu His His Asn Thr	
70 75 80	
CAG ACC TTC CAA GGC CCT CAT GCT GTA AAG AAG TTG AGT TCT GGA AAC	447
Gln Thr Phe Gln Gly Pro His Ala Val Lys Lys Leu Ser Ser Gly Asn	
85 90 95 100	
TCC AAG TTA TCA TCG TCC AAG TTT AGC AAT CCC ATC AGC AGC AGC AAG	495
Ser Lys Leu Ser Ser Ser Lys Phe Ser Asn Pro Ile Ser Ser Ser Lys	
105 110 115	
AGG AAT GTC TCC CTC CTG ATA TCA GCT AAT TCA GGA CTG TGAGCCGGCT	544
Arg Asn Val Ser Leu Leu Ile Ser Ala Asn Ser Gly Leu	

03374450-051697

65

125

(2) INFORMATION FOR SEQ ID NO.2:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:2:

Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys Phe
95 100 105

Ser Asn Pro Ile Ser Ser Ser Lys Arg Asn Val Ser Leu Leu Ile Ser
110 115 120

Ala Asn Ser Gly Leu
125

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Thr Glu Thr Lys Glu Val Gln Ser Ser Leu Lys Ala Gln Gln Gly
1 5 10 15
Leu Glu Ile Glu Met Phe His Met Gly Phe Gln Asp Ser Ser Asp Cys
20 25 30
Cys Leu Ser Tyr Asn Ser Arg Ile Gln Cys Ser Arg Phe Ile Gly Tyr
35 40 45
Phe Pro Ile Ser Gly Gly Cys Thr Arg Pro Gly Ile Ile Phe Ile Ser
50 55 60
Lys Arg Gly Phe Gln Val Cys Ala Asn Pro Ser Asp Arg Arg Val Gln
65 70 75 80
Arg Cys Arg Leu Glu Gln Asn Ser Gln Pro Arg Thr Tyr Lys Gln
85 90 95

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCCGTCGACG TCCACACCCA AGGTGTC

67

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCCTCTAGAG GAGCCCAGAA ATGAGCCGGC

30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCCTCTAGAG CCATCATGAA CCTGTGGCTC CTGGCC

36

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCTCTAGAG GAGCCCAGAA ATGACCCGGC

30

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs

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(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGAAGCTTA TGAACCTGTG GCTCCTGGCC

30

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCTCGAGT CAAGCGTAGT CTGGGACGTC GTATGGGTAC AGTCCTGAAT TAGCTGATAT

60

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61

00074460 051597 259750 09442880

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